



AKT3-5001-C1 Substitute Seq Listing.ST25
SEQUENCE LISTING

<110> Takeda San Diego, Inc.

<120> CRYSTALLIZATION OF AKT3

<130> AKT3-5001-C1

<140> 10/601,311

<141> 2003-06-20

<150> 60/400,207

<151> 2002-07-31

<160> 4

<170> PatentIn version 3.3

<210> 1

<211> 479

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(479)

<223> Amino acid sequence for full length human wild type AKT3

<300>

<308> Genbank/NP_005456

<309> 2002-04-04

<313> (1)..(461)

<400> 1

Met Ser Asp Val Thr Ile Val Lys Glu Gly Trp Val Gln Lys Arg Gly
1 5 10 15

Glu Tyr Ile Lys Asn Trp Arg Pro Arg Tyr Phe Leu Leu Lys Thr Asp
20 25 30

Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro
35 40 45

Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr
50 55 60

Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr
65 70 75 80

Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu
85 90 95

Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln
100 105 110

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Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile
115 120 125

Gly Glu Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr
130 135 140

Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly
145 150 155 160

Lys Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met
165 170 175

Lys Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His
180 185 190

Thr Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu
195 200 205

Thr Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val
210 215 220

Met Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu
225 230 235 240

Arg Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val
245 250 255

Ser Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu
260 265 270

Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr
275 280 285

Asp Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys
290 295 300

Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp
305 310 315 320

Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met
325 330 335

Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu
340 345 350

Lys Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr
355 360 365

AKT3-5001-C1 Substitute Seq Listing.ST25

Leu Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp
370 375 380

Pro Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met
385 390 395 400

Arg His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys
405 410 415

Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr
420 425 430

Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro
435 440 445

Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg
450 455 460

Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu
465 470 475

<210> 2
<211> 978
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(978)
<223> Human CDNA sequence encoding residues 136-461 of AKT3

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aaaggcactt ttgggaaagt tatttttggt cgagagaagg caagtggaaa atactatgct 120
atgaagattc tgaagaaaga agtcattatt gcaaaggatg aagtggcaca cactctaact 180
gaaagcagag tattaaagaa cactagacat ccctttttaa catccttgaa atattccttc 240
cagacaaaag accgtttgtg ttttgtgatg gaatatgtta atgggggcga gctgtttttc 300
catttgtcga gagagcgggt gttctctgag gaccgcacac gtttctatgg tgcagaaatt 360
gtctctgcct tggactatct acattccgga aagatttgtt accgtgatct caagttggag 420
aatctaattg tggacaaaga tggccacata aaaattacag attttggact ttgcaaagaa 480
gggatcacag atgcagccac catgaagaca ttctgtggca ctccagaata tctggcacca 540
gaggtgttag aagataatga ctatggccga gcagtagact ggtggggcct aggggttgtc 600
atgtatgaaa tgatgtgtgg gaggttacct ttctacaacc aggaccatga gaaacttttt 660

AKT3-5001-C1 Substitute Seq Listing.ST25

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gaattaatat taatggaaga cattaaattt cctcgaacac tctcttcaga tgcaaaatca 720
ttgcttttcag ggctcttgat aaaggatcca aataaacgcc ttggtggagg accagatgat 780
gcaaaagaaa ttatgagaca cagtttcttc tctggagtaa actggcaaga tgtatatgat 840
aaaaagcttg tacctccttt taaacctcaa gtaacatctg agacagatac tagatatttt 900
gatgaagaat ttacagctca gactattaca ataacaccac ctgaaaaata tgatgaggat 960
ggtatggact gcatggac 978

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<210> 3
<211> 556
<212> PRT
<213> Artificial

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<220>
<223> Amino acid sequence for residues 136-461 of AKT3 with a cleavable
      intein tag and cleavage site

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<220>
<221> MISC_FEATURE
<222> (1)..(226)
<223> Cleavable N-terminal intein tag

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<220>
<221> MISC_FEATURE
<222> (227)..(230)
<223> CRSL cleavage site

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<220>
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<222> (231)..(556)
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<400> 3

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Met Lys Ile Glu Glu Gly Lys Leu Thr Asn Pro Gly Val Ser Ala Trp
1          5          10          15

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Gln Val Asn Thr Ala Tyr Thr Ala Gly Gln Leu Val Thr Tyr Asn Gly
20          25          30

```

```

Lys Thr Tyr Lys Cys Leu Gln Pro His Thr Ser Leu Ala Gly Trp Glu
35          40          45

```

```

Pro Ser Asn Val Pro Ala Leu Trp Gln Leu Gln Asn Asn Gly Asn Asn
50          55          60

```

```

Gly Leu Glu Leu Arg Glu Ser Gly Ala Ile Ser Gly Asp Ser Leu Ile
65          70          75          80

```

```

Ser Leu Ala Ser Thr Gly Lys Arg Val Ser Ile Lys Asp Leu Leu Asp
85          90          95

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AKT3-5001-C1 Substitute Seq Listing.ST25

Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys Leu
 100 105 110
 Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu Val
 115 120 125
 Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala Asn
 130 135 140
 His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu Ser
 145 150 155 160
 Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser Leu
 165 170 175
 Gln Leu Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile Tyr Trp
 180 185 190
 Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val Phe Asp
 195 200 205
 Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile Ile Val
 210 215 220
 His Asn Cys Arg Ser Leu Ser Thr Thr His His Lys Arg Lys Thr Met
 225 230 235 240
 Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys
 245 250 255
 Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met Lys
 260 265 270
 Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr
 275 280 285
 Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu Thr
 290 295 300
 Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val Met
 305 310 315 320
 Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg
 325 330 335
 Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val Ser
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AKT3-5001-C1 Substitute Seq Listing.ST25

340

345

350

Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu Lys
355 360 365

Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp
370 375 380

Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys Thr
385 390 395 400

Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn
405 410 415

Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr
420 425 430

Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys
435 440 445

Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr Leu
450 455 460

Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp Pro
465 470 475 480

Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met Arg
485 490 495

His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys Lys
500 505 510

Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg
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Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro Pro
530 535 540

Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp
545 550 555

<210> 4
<211> 330
<212> PRT
<213> Artificial

<220>
<223> CRSL fused to the N-terminal of amino acid residues 136-461 of AKT3

AKT3-5001-C1 Substitute Seq Listing.ST25

<220>
 <221> MISC_FEATURE
 <222> (1)..(4)
 <223> CRSL cleavage site

<220>
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 <222> (5)..(330)
 <223> Amino acid sequence for residues 136-461 of AKT3

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Cys Arg Ser Leu Ser Thr Thr His His Lys Arg Lys Thr Met Asn Asp
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Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile
 20 25 30

Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met Lys Ile Leu
 35 40 45

Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr Leu Thr
 50 55 60

Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu Thr Ser Leu
 65 70 75 80

Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val Met Glu Tyr
 85 90 95

Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe
 100 105 110

Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu
 115 120 125

Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu Lys Leu Glu
 130 135 140

Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly
 145 150 155 160

Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys Thr Phe Cys
 165 170 175

Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr
 180 185 190

Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met

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195

200

205

Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu Phe
 210 215 220

Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr Leu Ser Ser
 225 230 235 240

Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp Pro Asn Lys
 245 250 255

Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met Arg His Ser
 260 265 270

Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys Lys Leu Val
 275 280 285

Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe
 290 295 300

Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro Pro Glu Lys
 305 310 315 320

Tyr Asp Glu Asp Gly Met Asp Cys Met Asp
 325 330

AKT3-5001-C1 Substitute Seq Listing.ST25
SEQUENCE LISTING

<110> Takeda San Diego, Inc.
<120> CRYSTALLIZATION OF AKT3
<130> AKT3-5001-C1
<140> 10/601,311
<141> 2003-06-20
<150> 60/400,207
<151> 2002-07-31
<160> 4
<170> PatentIn version 3.3
<210> 1
<211> 479
<212> PRT
<213> Homo sapiens

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<223> Amino acid sequence for full length human wild type AKT3

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<309> 2002-04-04
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20 25 30
Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro
35 40 45
Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr
50 55 60
Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr
65 70 75 80
Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu
85 90 95
Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln
100 105 110

AKT3-5001-C1 Substitute Seq Listing.ST25

Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile
 115 120 125
 Gly Glu Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr
 130 135 140
 Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly
 145 150 155 160
 Lys Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met
 165 170 175
 Lys Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His
 180 185 190
 Thr Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu
 195 200 205
 Thr Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val
 210 215 220
 Met Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu
 225 230 235 240
 Arg Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val
 245 250 255
 Ser Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu
 260 265 270
 Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr
 275 280 285
 Asp Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys
 290 295 300
 Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp
 305 310 315 320
 Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met
 325 330 335
 Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu
 340 345 350
 Lys Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr
 355 360 365

AKT3-5001-C1 Substitute Seq Listing.ST25

Leu Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp
370 375 380

Pro Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met
385 390 395 400

Arg His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys
405 410 415

Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr
420 425 430

Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro
435 440 445

Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg
450 455 460

Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu
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<210> 2
<211> 978
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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<223> Human cDNA sequence encoding residues 136-461 of AKT3

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aaaggcactt ttgggaaagt tatttttggt cgagagaagg caagtggaaa atactatgct 120
atgaagattc tgaagaaaga agtcattatt gcaaaggatg aagtggcaca cactctaact 180
gaaagcagag tattaagaa cactagacat ccctttttaa catccttgaa atattccttc 240
cagacaaaag accgtttgtg ttttgtgatg gaatatgtta atgggggcga gctgtttttc 300
catttgtcga gagagcgggt gttctctgag gaccgcacac gtttctatgg tgcagaaatt 360
gtctctgcct tggactatct acattccgga aagattgtgt accgtgatct caagttggag 420
aatctaattgc tggacaaaga tggccacata aaaattacag attttggact ttgcaaagaa 480
gggatcacag atgcagccac catgaagaca ttctgtggca ctccagaata tctggcacca 540
gaggtgttag aagataatga ctatggccga gcagtagact ggtggggcct aggggttgtc 600
atgtatgaaa tgatgtgtgg gaggttacct ttctacaacc aggaccatga gaaacttttt 660

AKT3-5001-C1 Substitute Seq Listing.ST25

gaattaatat taatggaaga cattaaattt cctcgaacac tctcttcaga tgcaaaatca	720
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gcaaaagaaa ttatgagaca cagtttcttc tctggagtaa actggcaaga tgtatatgat	840
aaaaagcttg tacctccttt taaacctcaa gtaacatctg agacagatac tagatatttt	900
gatgaagaat ttacagctca gactattaca ataacaccac ctgaaaaata tgatgaggat	960
ggtatggact gcatggac	978

<210> 3
 <211> 556
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence for residues 136-461 of AKT3 with a cleavable intein tag and cleavage site

<220>
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 <222> (1)..(226)
 <223> Cleavable N-terminal intein tag

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<220>
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 <223> Amino acid sequence for resisues 136-461 of AKT3

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Met	Lys	Ile	Glu	Glu	Gly	Lys	Leu	Thr	Asn	Pro	Gly	Val	Ser	Ala	Trp
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Gln	Val	Asn	Thr	Ala	Tyr	Thr	Ala	Gly	Gln	Leu	Val	Thr	Tyr	Asn	Gly
			20					25					30		

Lys	Thr	Tyr	Lys	Cys	Leu	Gln	Pro	His	Thr	Ser	Leu	Ala	Gly	Trp	Glu
		35					40					45			

Pro	Ser	Asn	Val	Pro	Ala	Leu	Trp	Gln	Leu	Gln	Asn	Asn	Gly	Asn	Asn
	50					55					60				

Gly	Leu	Glu	Leu	Arg	Glu	Ser	Gly	Ala	Ile	Ser	Gly	Asp	Ser	Leu	Ile
65					70					75					80

Ser	Leu	Ala	Ser	Thr	Gly	Lys	Arg	Val	Ser	Ile	Lys	Asp	Leu	Leu	Asp
				85					90					95	

AKT3-5001-C1 Substitute Seq Listing.ST25

Glu Lys Asp Phe Glu Ile Trp Ala Ile Asn Glu Gln Thr Met Lys Leu
100 105 110

Glu Ser Ala Lys Val Ser Arg Val Phe Cys Thr Gly Lys Lys Leu Val
115 120 125

Tyr Ile Leu Lys Thr Arg Leu Gly Arg Thr Ile Lys Ala Thr Ala Asn
130 135 140

His Arg Phe Leu Thr Ile Asp Gly Trp Lys Arg Leu Asp Glu Leu Ser
145 150 155 160

Leu Lys Glu His Ile Ala Leu Pro Arg Lys Leu Glu Ser Ser Ser Leu
165 170 175

Gln Leu Ser Pro Glu Ile Glu Lys Leu Ser Gln Ser Asp Ile Tyr Trp
180 185 190

Asp Ser Ile Val Ser Ile Thr Glu Thr Gly Val Glu Glu Val Phe Asp
195 200 205

Leu Thr Val Pro Gly Pro His Asn Phe Val Ala Asn Asp Ile Ile Val
210 215 220

His Asn Cys Arg Ser Leu Ser Thr Thr His His Lys Arg Lys Thr Met
225 230 235 240

Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys
245 250 255

Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met Lys
260 265 270

Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr
275 280 285

Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu Thr
290 295 300

Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val Met
305 310 315 320

Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg
325 330 335

Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val Ser
Page 5

AKT3-5001-C1 Substitute Seq Listing.ST25

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345

350

Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu Lys
355 360 365

Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp
370 375 380

Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys Thr
385 390 395 400

Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn
405 410 415

Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr
420 425 430

Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys
435 440 445

Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr Leu
450 455 460

Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp Pro
465 470 475 480

Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met Arg
485 490 495

His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys Lys
500 505 510

Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg
515 520 525

Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro Pro
530 535 540

Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp
545 550 555

<210> 4

<211> 330

<212> PRT

<213> Artificial

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<223> CRSL fused to the N-terminal of amino acid residues 136-461 of AKT3

AKT3-5001-C1 Substitute Seq Listing.ST25

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 <222> (1)..(4)
 <223> CRSL cleavage site

<220>
 <221> MISC_FEATURE
 <222> (5)..(330)
 <223> Amino acid sequence for residues 136-461 of AKT3

<400> 4

Cys Arg Ser Leu Ser Thr Thr His His Lys Arg Lys Thr Met Asn Asp
 1 5 10 15

Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly Lys Val Ile
 20 25 30

Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met Lys Ile Leu
 35 40 45

Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His Thr Leu Thr
 50 55 60

Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu Thr Ser Leu
 65 70 75 80

Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val Met Glu Tyr
 85 90 95

Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu Arg Val Phe
 100 105 110

Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val Ser Ala Leu
 115 120 125

Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu Lys Leu Glu
 130 135 140

Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr Asp Phe Gly
 145 150 155 160

Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys Thr Phe Cys
 165 170 175

Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp Asn Asp Tyr
 180 185 190

Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met Tyr Glu Met

AKT3-5001-C1 Substitute Seq Listing.ST25

195

200

205

Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu Lys Leu Phe
 210 215 220

Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr Leu Ser Ser
 225 230 235 240

Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp Pro Asn Lys
 245 250 255

Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met Arg His Ser
 260 265 270

Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys Lys Leu Val
 275 280 285

Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr Arg Tyr Phe
 290 295 300

Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro Pro Glu Lys
 305 310 315 320

Tyr Asp Glu Asp Gly Met Asp Cys Met Asp
 325 330